Appendix I

Please help us to better understand your needs and expectations regarding ExPASy and complete our online survey!

Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: SeqID4, (226 residues)
Sequence 2: E.coli, (226 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

```
68.5% identity in 216 residues overlap; Score: 745.0; Gap frequency: 0.0%

SeqID4,       9 RLCRTLGYEFNNIELLIQALTHRSAANKHNERLEFLGDSILSIAISDALYHQFPKATEGD
E.coli,       8 RLQRKLGYTFNHQELLQQALTHRSASSKHNERLEFLGDSILSYVIANALYHRFPRVDEGD
                ** * *** **  *** ********  ***************  * **** **   ***

SeqID4,      69 LSRMRATLVKGDTLTIIAKEFKLGDYLYLGPGELKSGGFRRESILADAVEAIIGAVYLDA
E.coli,      68 MSRMRATLVRGNTLAELAREFELGECLRLGPGELKSGGFRRESILADTVEALIGGVFLDS
                ******** * **   * ** **  * ********************* *** ** * **

SeqID4,     129 DIEVCRKLLLSWYQERLAEIKPGINQKDPKTILQEYLQGFKKPLPDYQVVAVEGEAHDQT
E.coli,     128 DIQTVEKLILNWYQTRLDEISPGDKQKDPKTRLQEYLQGRHLPLPTYLVVQVRGEAHDQE
                **    ** * *** ** ** **  ****** *******   *** * ** * ******

SeqID4,     189 FTVECKISELDKVVTGVASSRRKAEQLAAAQVLELL
E.coli,     188 FTIHCQVSGLSEPVVGTGSSRRKAEQAAAEQALKKL
                **  *  * *   * *  ******** ** * *  *

---

35.3% identity in 17 residues overlap; Score: 24.0; Gap frequency: 0.0%

SeqID4,     104 SGGFRRESILADAVEAI
E.coli,     204 TGSSRRKAEQAAAEQAL
                 *  **    * *  *

---

41.7% identity in 12 residues overlap; Score: 22.0; Gap frequency: 0.0%
```